

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:48:26 ; Search time 27.34 Seconds

(without alignments)
36.221 Million cell updates/sec

Title: US-09-432-546-4
Perfect score: 99
Sequence: 1 RRPMPMPKXPLI 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62.6	144	1	JC1222	indolicidin precursor
2	57.6	166	2	T18540	motA protein precursor
3	56.6	236	2	F83705	hypothetical protein
4	55.6	236	2	J00606	arylsulfatase (EC 3
5	53.5	95	2	E86447	protein FSD14.5 [I
6	52.5	970	2	C84488	hypothetical protein
7	52.5	1231	2	C84716	hypothetical protein
8	52.5	301	2	G83556	hypothetical protein
9	52.5	1112	2	S70522	cyclic nucleotide
10	51.5	196	2	B48332	cysteine-rich exte
11	51.5	209	2	A48232	hypothetical prote
12	51.5	321	2	F84611	hypothetical prote
13	51.5	498	1	UT0751	ferredoxin--NADP+
14	51.5	2970	2	T08639	polyprotein - marm
15	51.5	1173	1	VG1HHC	E2 glycoprotein pr
16	50.5	279	2	S68239	photosynthetic rea
17	50.5	279	2	E49964	photosynthetic rea
18	50.5	279	2	T50889	photosynthetic rea
19	50.5	560	2	T32661	hypothetical prote
20	50.5	83	2	B72392	hypothetical prote
21	49.5	50.0	253	G70715	hypothetical prote
22	49.5	50.0	257	S70177	hypothetical prote
23	49.5	50.0	497	A40487	ferredoxin--NADP+
24	49.5	169	2	F72532	hypothetical prote
25	49.5	456	1	T40516	spar protein - Bac
26	49.5	669	2	T28028	hypothetical prote
27	48.5	49.0	212	S57330	cathelin-like anti
28	48.5	49.0	228	S40463	prophenin (Pr-2) p
29	48.5	314	2	H84677	hypothetical prote

ALIGNMENTS

30	48	48.5	947	2	H85088	hypothetical prote
31	48	48.5	990	1	G46335	env polypeptide pr
32	48	48.5	1172	2	F96503	hypothetical prote
33	47.5	48.0	111	2	T29295	hypothetical prote
34	47.5	48.0	248	2	S23449	NADH oxidase (H202
35	47.5	48.0	752	2	E82146	Rec2-related prote
36	47	47.5	73	2	D75497	hypothetical prote
37	47	47.5	212	2	P00518	envelope protein -
38	47	47.5	233	2	B96652	protein F23N19.5 [
39	47	47.5	253	2	D86310	protein FIL3.4 [Im
40	47	47.5	299	2	T12505	hypothetical prote
41	47	47.5	964	1	VCLJC6	env polypeptide pr
42	47	47.5	966	1	VCLJJC	env polypeptide pr
43	47	47.5	982	1	VCLJVS	env polypeptide pr
44	47	47.5	983	1	E45390	env polypeptide pr
45	47	47.5	1055	2	A96682	protein F1E22.12 [

RESULT 1

JC1222

indolicidin precursor - bovine

N:Alternate names: antimicrobial peptide

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JC1222; A42387; S25664

R:del Sal, G.; Storici, P.; Schneider, C.; Romeo, D.; Zanetti, M.

Biochem. Biophys. Res. Commun. 187, 467-472, 1992

A:Title: CDNA cloning of the neutrophil bactericidal peptide indolicidin.

A:Reference number: JC1222; MUID:92392368

A:Accession: JC1222

A:Molecule type: mRNA

A:Residues: 1-144 <SAL>

A:Cross-references: EMBL:X67340; NID:9462; PIDD:CAA47755.1; PID:9463

A:Experimental source: Bone marrow

J:Seidel, M.E.; Novotny, M.J.; Morris, W.L.; Tang, Y.Q.; Smith, W.; Cullor, J.S.

J: Biol. Chem. 267, 4292-4295, 1992

A:Title: Indolicidin, a novel bactericidal tridecapeptide amide from neutrophils.

A:Reference number: A42387; MUID:92165771

A:Accession: A42387

A:Molecule type: protein

A:Residues: 131-143 <SEL>

A:Experimental source: neutrophils

A:Note: Sequence extracted from NCBI backbone (NCBIP:83840)

C:Superfamily: cathelin; cystatin homology

C:Keywords: amidated carboxyl end

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-130/Domain: cystatin homology <CYS>

F:131-143/Product: indolicidin #status experimental <PRO>

F:143/Modified site: amidated carboxyl end (Arg) (amide in mature form from following

Query Match 62.6%; Score 62; DB 1; Length 144;

Best Local Similarity 75.0%; Pred. No. 0.24;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRPMPMPK 9

DB 135 KRPMPMPK 142

RESULT 2

T18540

moA protein precursor [imported] - Leptothrix discophora

C:Species: Leptothrix discophora

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2000

C:Accession: T18540

R:Corstjens, P.L.

submitted to the EMBL Data Library, April 1999

A:Reference number: Z18959

A:Accession: T18540
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1662 <COR>
A:Cross-references: EMBL:Z25774; NID:el427784; PID:e267517; PIDN:CAA81037.1
A:Note: moFA
F:1-33/Domains: signal sequence #status predicted <SIG>
F:43-1662/Product: moFA protein #status predicted <MAT>

Query Match 57.6%; Score 57; DB 2; Length 1662;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 RWPMPWKWPL 12
|||
Db 490 RWMGPFMPV 500

RESULT 3
F83705
hypothetical protein BH0446 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: F83705
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20263314
A:Accession: F83705
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-236 <STO>
A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04165.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0446

Query Match 56.6%; Score 56; DB 2; Length 236;
Best Local Similarity 77.8%; Pred. No. 2.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 WMPWKWPL 13
|||||
Db 192 WLPWKWPL 200

RESULT 4
JQ0606
arylesterase (EC 3.1.1.2) precursor - Pseudomonas fluorescens
C:Species: Pseudomonas fluorescens
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Mar-2000
C:Accession: JQ0606
R:Choi, K.D.; Jeon, G.H.; Rhee, J.S.; Yoo, O.J.
Agric. Biol. Chem. 54, 2039-2045, 1990
A:Title: Cloning and nucleotide sequence of an esterase gene from Pseudomonas fluorescens
A:Reference number: JQ0606; MUID:91182405
A:Accession: JQ0606
A:Molecule type: DNA
A:Residues: 1-236 <CHO>

A:Cross-references: GB:D12484; GB:D01134; NID:g216856; PIDN:BA02052.1; PID:d1002534; PI
A:Note: part of this sequence, including the amino end of the mature protein, was confir
C:Keywords: carboxylic ester hydrolase
F:2-236/Product: arylesterase #status predicted <MAT>

Query Match 55.6%; Score 55; DB 2; Length 236;
Best Local Similarity 44.4%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY 1 RRM-----PWWPKWPL 12

Db 205 RTWPRSTYPPWYPMWRRL 222
|||||

RESULT 5
E86447
protein F5D14.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E86447
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E86447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <STO>
A:Cross-references: GB:AE005172; NID:g8920603; PIDN:AE81325.1; GSPDB:GN00141
C:Genetics:
A:Gene: F5D14.5
A:Map position: 1

Query Match 53.5%; Score 53; DB 2; Length 95;
Best Local Similarity 29.6%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 3; Indels 14; Gaps 1;

OY 1 RRMWMP-----WKWPL 13
|||||
Db 59 RWMWMPVLVITDVGGEMSWMWMPVL 85

RESULT 6
C84488
hypothetical protein At2g07730 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84488
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-970 <STO>

A:Cross-references: GB:AB002093; NID:g3327392; PIDN:AC26674.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g07730
A:Map position: 2

Query Match 53.0%; Score 52.5; DB 2; Length 970;
Best Local Similarity 46.7%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

OY 3 WP-----WMPWKW 10
|||
Db 739 WPTLSMGIWMAWKW 753

RESULT 7
C84716

Hypothetical protein Atcg31080 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: C84716
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shear, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vannken, S.E.; Umagam, L.; Tallon, L.;
 euss, D.; Niemann, W.C.; White, O.; Eisten, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MIMD:20083487
 A:Accession: C84716
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1231 <STO>
 A:Cross-references: GB:AE002093; NID:g3746069; PIDN:AAC63844.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: Atcg31080
 A:Map position: 2

```

Query Match      Score 53.5; DB 2: length 1231;
Best Local Similarity 46.7%;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1.
OY 3 WP-----WPPWKW 10
    |||
Db 1000 WPTLFGMGITWNAWKW 1014

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RESULT      8
GB3556
hypothetical protein PA0702 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: GB3556
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
aman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardy, K.; Lim,
. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: GB3556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1,301 <STO>
A:Cross-references: GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AA04091.1; GSPDB:GN003
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0702

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Query Match	52.5%	Score 52	DB 2	Length 301
Best Local Similarity	70.0%	Pred. No. 8.3		
Matches 7	Conservative	0	Mismatches 3	Indels 0
Gaps 0				
Oy	3 WPMWPMKMP	12		
Db	97 WPMWPMKMP	106		

RESULT 9
S70522
cyclic nucleotide phosphodiesterase, cGMP-inhibited (EC 3.1.4.-) - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 19-May-2000
C:Accession: S70522
R:Murata, T.; Taira, M.; Manganiello, V.C.
FEBS Lett. 390, 29-33, 1996
A:Title: Differential expression of cGMP-inhibited cyclic nucleotide phosphodiesterases
A:Reference number: S70522; MUID:96314543
A:Accession: S70522
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA

A:Residues: 1-1112 <MUR>
A:Cross-references: EMBL:U38178; NTD:G145301; PID:G1445302
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
C:Superfamily: cyclic-nucleotide phosphodiesterase, cGMP-inhibited, 3',5'-cyclic-nucleotide phosphoric diester hydrolase
C:Keywords: phosphoric diester hydrolase
F:736-1006/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match	52.5%;	Score 52;	DB 2;	Length 1112;
Best Local Similarity	62.5%;	Pred. No. 29;		
Matches	5;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	3	WPPWPKKY	10	
	1	1	1	1
Db	169	WQWNSWPM	176	

RESULT 10
B48232
cysteine-rich extensin-like protein 2 precursor - common tobacco
C.Species: *Nicotiana tabacum* (common tobacco)
C.Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C.Accession: B48232; P00474; S24616
R.Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A.Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A.Reference number: A48232; MUID:93342083
A.Accession: B48232

A:Residues: 1196 <MOD>
A:Cross-references: GB:LI3440; NID:9310924; PIDN:AA34060.1; PID:9310925
R:Ride S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A:Title: Developmental expression of tobacco pistil-specific genes encoding novel ex
A:Reference number: PQ0474; MUID:93005740
A:Accession: PQ0474
A:Molecule type: mRNA
A:Residues: 'MAG',1-105 <GOL>
A:Cross-references: EMBL:Z14014
A:Experimental source: stigma, style; strain Petit Havana SRI
C:Genetics:
A:Gene: CELP-2
C:Superfamily: glutelin
C:Keywords: cell wall; extracellular matrix; fertilization
F:1-19/Domain: signal sequence #status predicted <SIS>
F:20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>

Query Match	Similarity	52.0%	Score 51.5;	DB 2;	Length 196;
Best Local	Similarity	43.8%	Pred. No. 6.3;		
Matches	7; Conservative	1;	Mismatches	1;	Indels 7; Gaps 1.
QY	3 WPW-----WPKWKP	11			
Db	40 WPEWIPCYLTWPEPP	55			

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RESULT 11
A48232
cysteine-rich extensin-like protein 1 precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C:Accession: A48232; P00475; S24617
R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A:Reference number: A48232, MID:93342083
A:Accession: A48232
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-209 <MDA>
A:Cross-references: GB:113439; NID:g310922; PIDN:AAA34059.1; PID:g310923

```

R.de S Goldman, M.H.; Pezzotti, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992
A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin
A:Reference number: P00474; MID:93005740
A:Accession: P00475

A:Molecule type: mRNA
A:Residues: 39-209 <GOL>
A:Cross-references: EMBL:214020; NID:g19918; PID:g19919
A:Experimental source: stigma, style; strain Petit Havana SRI
A:Superfamily: glutelin
C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
F:146/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
Best Local Similarity 52.0%; Score 51.5; DB 2; Length 209;
Matches 7; Conservative 1; Mismatches 1; Indels 7; Gaps 1;

QY 3 WP-----WPKWP 11
DB 45 WPEIPCYLTWPFMP 60

RESULT 12

FE4611
Hypothetical protein Atg22350 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

A:Accession: FE4611

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, L.
-Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MID:20083487

A:Accession: FE4611

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-321 <STO>

A:Cross-references: GB:AE002093; NID:g4544460; PIDN:AA22368.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg22350

A:Map position: 2

Query Match
Best Local Similarity 52.0%; Score 51.5; DB 2; Length 321;
Matches 7; Conservative 0; Mismatches 1; Indels 7; Gaps 1;

QY 3 WP-----WPKWP 10
DB 90 WPTVFVAVVWGMKW 104

RESULT 13

JT0751

ferredoxin--NADP+ reductase (BC 1.18.1.2), long form precursor - bovine

N:Alternate names: adrenodoxin reductase

C:Species: Bos primigenius taurus (cattle)

C:Date: 14-Jul-1994 #sequence_revision 18-Oct-1996 #text_change 16-Jun-2000

C:Accession: JT0751; JT0079; JS0390; S03558; PS0003; A23604; S52100

R:Taketa, Y.; Sagata, Y.; Kono, A.; Sekimizu, K.; Horinuchi, T.

Biol. Pharm. Bull. 16, 1200-1206, 1993

A:Title: Gene structure of bovine adrenodoxin reductase.

A:Reference number: JT0751; MID:94177140

A:Accession: JT0751

A:Molecule type: DNA

A:Residues: 1-498 <TAK>

A:Cross-references: GB:D83475; NID:g1199916; PIDN:BA11921.1; PID:g4521308

A:Experimental source: adrenal cortex
A:Note: the authors translated the codon GTC for residue 205 as GLY

R:Sagara, Y.; Takata, Y.; Miyata, T.; Hara, T.; Horinuchi, T.

J. Biochem. 102, 1333-1336, 1987

A:Title: Cloning and sequence analysis of adrenodoxin reductase cDNA from bovine adrenal cortex

A:Reference number: JT0079; MID:88198050

A:Accession: JT0079

A:Molecule type: mRNA

A:Residues: 1-204, 211-498 <SAG>

A:Cross-references: GB:000211; NID:g217433; PIDN:BA00150.1; PID:g217434

A:Note: the deduced sequence is partially confirmed by amino acid sequencing of 15 is

R:Sagara, Y.

submitted to DDBJ, September 1989

A:Reference number: JS0390

A:Contents: revision, insertion of residues 205-210

A:Accession: JS0390

A:Molecule type: mRNA

A:Residues: 56-498 <SAG>

R:Hannukoglu, I.; Gutfinger, T.

Eur. J. Biochem. 180, 479-484, 1989

A:Title: cDNA sequence of adrenodoxin reductase. Identification of NADP-binding sites

A:Reference number: S03558; MID:89170752

A:Accession: S03558

A:Molecule type: mRNA

A:Residues: 155-204, 211-498 <HAN>

A:Cross-references: EMBL:X13736; NID:g65; PIDN:CAA32002.1; PID:g833776

A:Note: 405-Ser was also found

R:Hamamoto, I.; Kurokouchi, K.; Tanaka, S.; Ichikawa, Y.

Biochim. Biophys. Acta 953, 207-213, 1988

A:Title: Adrenoferrredoxin-binding peptide of NADPH-adrenoferrredoxin reductase.

A:Reference number: PS0003; MID:88184054

A:Accession: PS0003

A:Molecule type: protein

A:Residues: 33-41, 'S', 43-62, 260-283, 'TW', 496-498 <HAM>

A:Note: a cyanogen bromide peptide binds to adrenoferrredoxin

R:Nonaka, Y.; Kurahashi, H.; Yabusa, Y.; Kuramitsu, S.; Kagamiyama, H.; Yamano, T.;

Biochem. Biophys. Res. Commun. 145, 1239-1247, 1987

A:Title: Molecular cloning and sequence analysis of full-length cDNA for mRNA of adre

A:Reference number: A29604; MID:87270696

A:Accession: A29604

A:Molecule type: mRNA

A:Residues: 1-76, 'R', 78-80, 'VWALTPRRSMIL', 95-123, 'RVYRLP', 129-204, 211-273, 'R', 275-3

A:Cross-references: GB:M17029; NID:g162628; PIDN:AAA30362.1; PID:g162629

A:Experimental source: adrenal cortex

R:Warburton, R.J.; Seybert, D.W.

Biochim. Biophys. Acta 1246, 39-46, 1995

A:Title: Structural and functional characterization of bovine adrenodoxin reductase b

A:Reference number: S52100; MID:95110846

A:Accession: S52100

A>Status: preliminary

A:Molecule type: protein

A:Residues: 'X', 34-41, 'X', 43-48, 'X', 50-51, 304-306, 'X', 308-309, 'X', 311-326 <WAR>

A:Comment: ferredoxin--NADP+ reductase is localized in the matrix of adrenal cortex m

ferredoxin--NADP+ reductase, adrenodoxin and two forms of cytochrome P-450.

C:Genetics:

A:Insertions: 27/1; 59/3; 91/3; 132/3; 170/3; 204/3; 246/3; 275/1; 341/3; 399/1; 456/1

C:Function:

A:Description: catalyzes the reversible reduction of NADP+ by reduced ferredoxin or r

C:Superfamily: human ferredoxin--NADP+ reductase

C:Keywords: alternative splicing; flavoprotein; mitochondrion; monomer; NADP; oxidore

F:1-32/Domain: transit peptide (mitochondrion) #status predicted <SIG>

F:33-498/Product: ferredoxin--NADP+ reductase, long form #status predicted <MAT>

F:40-70/Region: beta-alpha-beta RND nucleotide-binding fold

F:180-190/Region: NADP binding #status predicted

F:281/Binding site: substrate (Lys) #status experimental

Query Match
Best Local Similarity 52.0%; Score 51.5; DB 1; Length 498;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 RRPWMPW-KW 10
DB 4 RCMRWMPWSSW 14

RESULT 14

T08839

polyprotein - marmoset hepatitis GB virus A

C:Species: marmoset hepatitis GB virus A

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000

C:Accession: T08839

R:Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K.

J. Gen. Virol. 79, 41-45, 1998

A:Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.

A:Reference number: Z16486; MUID:98120818

A:Accession: T08839

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: genomic RNA

A:Cross-references: EMBL:AF023424; NID:g2828597; PIDN:MAC40501.1; PID:g2828598

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: polyprotein

Query Match

Best Local Similarity 52.0%; Score 51.5; DB 2; Length 2970;

Matches 8; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 2 RWPWMP-----MKWP 11

DB 807 RWPWLPKMLVAWFWP 823

RESULT 15

VGIIHC

E2 glycoprotein precursor - human coronavirus (strain 229E)

N:Alternate names: peplomer glycoprotein; S glycoprotein; spike glycoprotein

-C:Species: human coronavirus

A>Note: host Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Jun-2000

C:Accession: A34766; S05460

R:Raabe, T.; Schelle-Prinz, B.; Siedell, S.G.

J. Gen. Virol. 71, 1065-1073, 1990

A:Title: Nucleotide sequence of the gene encoding the spike glycoprotein of human corona

A:Reference number: A34766; MUID:90264837

A:Accession: A34766

A:Molecule type: mRNA

A:Residues: 1-1173 <RAA>

A:Cross-references: EMBL:X16816; NID:g58926; PIDN:CAA34723.1; PID:g58927

A:Experimental source: strain 229E

R:Raabe, T.; Siedell, S.

Nucleic Acids Res. 17, 6387, 1989

A:Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique

A:Reference number: A34038; MUID:89366667

A:Accession: S05460

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1159-1173 <RA2>

A:Cross-references: EMBL:X15654; NID:g58921; PIDN:CAA33680.1; PID:g1334827

C:Superfamily: coronavirus E2 glycoprotein

C:Keywords: glycoprotein; transmembrane protein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-1173/Product: E2 glycoprotein #status predicted <MAT>

F:116-1138/Domain: transmembrane #status predicted <TMN>

F:23,62,98,147,171,176,220,243,326,333,440,464,518,538,542,568,581,587,663,671,930,1015,

Query Match 51.5%; Score 51; DB 1; Length 1173;

Best Local Similarity 71.4%; Pred. No. 41;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RWPWMPW 8

DB 1113 KWPWYV 1119

Thu Jan 31 11:07:39 2002

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